

AMENDMENTS TO THE CLAIMS:

The listing of claims will replace all prior versions, and listings of claims in the application:

LISTING OF CLAIMS:

1. (Currently Amended) A computerized method for identifying peaks corresponding to glycans from a mass spectrum, said method comprising:
receiving ~~not less than~~ at least one glycan spectrum from a mass spectrometer, wherein said ~~not less than~~ at least one glycan spectrum includes peaks having a measured mass;
assigning glycan identifications to said peaks by comparing said measured mass to known masses of a customized set of possible glycans in a monosaccharide set table; and
~~reporting~~ combining said peak assignments with cartoons which are symbolic representations of the glycans in the monosaccharide table;
creating a glycan report consisting of the cartoon representations of each corresponding peak; and
reporting to a user the combined peak assignments and cartoons in the form of the glycan report.
2. (Currently Amended) The method for identifying peaks corresponding to glycans according to claim 1, further comprising constructing a the monosaccharide set table having a plurality of monosaccharides comprising isomers of corresponding to the customized set of possible glycans.
3. (Currently Amended) The method for identifying peaks corresponding to glycans according to claim 2, wherein constructing said monosaccharide set table comprises:
constructing a glycan/monosaccharide set chart, wherein each row represents a set of monosaccharides, further representing a set of possible glycan isomers;
applying combination ranges for a mass of said monosaccharides;

developing a rule set generated from an initial set of archetypes entered into an associated directory of the cartoons, wherein said rules specify monosaccharide combination limitations;

eliminating each of said monosaccharide rows not satisfying said rule set; and computing glycan isomer and glycan isotope frequency based on isotope frequencies for H, C, O, and N and glycan isomer frequency.

4. (Currently Amended) The method for identifying peaks corresponding to glycans according to claim 1, wherein assigning glycan identifications comprises:

calibrating said received glycan spectrum by at least defining an acceptable tolerance based on the tolerance of the high-confidence peak identifications; and

matching isotopes from said monosaccharide set table to said peaks within the said glycan spectrum.

5. (Currently Amended) The method for identifying peaks corresponding to glycans according to claim 4, wherein calibrating a user calibrates said received glycan spectrum, ~~comprises setting said calibration explicitly.~~

6. (Currently Amended) The method for identifying peaks corresponding to glycans according to claim 4, wherein matching the isotopes with said peaks comprises:

selecting the isotope with the highest expected frequency for each said monosaccharide;

searching said spectrum for a peak within an acceptable tolerance of said isotope; and

selecting said peak having the best isotope envelope.

7. (Currently Amended) The method for identifying peaks corresponding to glycans according to claim 4, further comprising performing a quality assessment to determine the likelihood that said matching of said peaks is correct.

wherein said quality assessment is based on factors including proximity of the measured mass to theoretical mass, computation of isotope envelopes, and examination of $m-1$ peak, wherein when the peak occurs at $m-1$, the height of the peak is checked and peak height is an indication of confidence in the assignment, wherein said quality assessment determines the likelihood that said peak assignment is correct.

8. (Currently Amended) The method for identifying peaks corresponding to glycans according to claim 7, wherein performing said quality assessment comprises:

measuring proximity of said measured mass of for a selected peak to the theoretical mass of the glycan;

computing said isotope envelopes for labeled or nonlabeled isotopes; and
examining the peak height at a peak height mass minus one position.

9. (Original) The method for identifying peaks corresponding to glycans according to claim 4, further comprising performing spectrum combination, wherein said spectrum combination includes combining the information from a plurality of spectra.

10. (Currently Amended) The method for identifying peaks corresponding to glycans according to claim 1, wherein said reporting of said peak assignments comprises ~~not less than~~ at least one family report, wherein said the family comprises a sequence of spectrum peaks, wherein the label for each succeeding peak contains ~~not less than~~ at least one more monosaccharide than the label of the preceding peak.

11. (Currently Amended) The method for identifying peaks corresponding to glycans according to claim 1, wherein said glycan identifications comprise a plurality of cartoons, wherein said cartoons comprise symbolic representations of said rows from said monosaccharide table.

Claims 12-20 (Canceled)

21. (Currently Amended) An article of manufacture comprising:
a computer usable medium having computer readable program code embodied in said medium which, when said program code is executed by said computer causes said computer to perform method steps for identifying peaks corresponding to glycans from a mass spectrum, said method steps comprising:

i. ~~receiving not less than~~ at least one glycan spectrum from a mass spectrometer, wherein said ~~not less than~~ at least one glycan spectrum includes peaks having a measured mass;

ii. assigning glycan identifications to said peaks by comparing said measured mass to the masses of a customized set of possible glycans

iii. creating a glycan report consisting of the cartoon representations of each corresponding peak; and

iv. reporting said peak assignments using cartoons as a symbolic representation of rows in a monosaccharide table.

22. (New) A method for identifying peaks corresponding to glycans from a mass spectrum with an automatic computerized estimation of accuracy of glycan assignments, said method comprising:

customizing a database of possible glycans in consideration of the type of sample to be tested;

processing the sample of at least one glycan through a mass spectrometer, wherein a mass of the sample is measured;

identifying the at least one glycan present in the sample by comparing the measured mass of the sample to known masses of a customizable set of possible glycans in a monosaccharide table;

labeling the peaks in the resulting spectra with cartoons of the represented glycans;

assigning a confidence score relating to the accuracy of the glycan assignment;

creating a glycan report consisting of the cartoon representation of each

corresponding peak with the assigned confidence score; and
reporting to a user the combined peak assignments and cartoons in the
form of a glycan report.

23. (New) The method for identifying peaks corresponding to glycans according to claim 22, wherein said set of possible glycans is adjusted depending on the identity of the sample.

24. (New) The method for identifying peaks corresponding to glycans according to claim 22, wherein said spectrum is automatically calibrated by measuring the relative difference between the observed and predicted masses of at least one high confidence peak identification.

25. (New) The method for identifying peaks corresponding to glycans according to claim 24, wherein said spectrum is automatically calibrated by defining an acceptable tolerance based on the tolerance of the high-confidence peak assignments.

26. (New) The method for identifying peaks corresponding to glycans according to claim 24, wherein said at least one high confidence peak comprises:
at least one of the 200 highest peaks;
a mass (m) within a set tolerance of a theoretical glycan mass (m), in
which no significant peaks are positioned near $m-1$; and
an isotope envelope closely matching the theoretical one.

27. (New) The method of claim 22, wherein an assignment is accepted if the observed mass and theoretical mass of the glycan satisfy

$$\left| \frac{\text{observed} - \text{theoretical} - a}{\text{theoretical}} \right| < b$$

where a and b are obtained by taking a high-confidence peak identifications and the measured relative difference between observed and predicted masses.

28. (New) The method of claim 23, wherein the relative " Δ " difference between a theoretical and observed peak is:

$$\Delta = \left| \frac{\textit{observed} - \textit{theoretical} - a}{\textit{theoretical}} \right|.$$